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New Bio-Informatics Software Allows for Interactive, Real-Time Analysis of Sequence Data

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DNA information is converted into RNA transcripts that serve many biological functions, instructions for making proteins. RNA is an essential product of the genome and directly responsible for which and how much protein is made in each cell of our bodies. (Darryl Leja, National Human Genome Research Institute)

SILVER SPRING, Md. — Researchers from the Naval Medical Research Center (NMRC), in collaboration with the Los Alamos National Laboratory, developed, tested and deployed to the field a unique software package. EDGE, short for *Empowering the Development of Genomics Expertise*, is designed to lower the barrier of bioinformatics, both in terms of hardware and ease of use.

The field of DNA sequencing has seen a lot of technological and scientific advancement since its discovery in the 1970's. Because of these advancements, what used to take days can now be done by a single technician in one day's time. EDGE is designed to analyze sequencing data and compile a detailed taxonomic profile from complex clinical or environmental samples containing bacteria and viruses. Results gathered on EDGE are available real-time as both static and interactive graphics.

"Not only has output increased, but preparation time and cost per base have decreased, and the physical footprint of a gene sequencing instrument in the laboratory is also dramatically decreasing, from being as large as a person to something small enough to fit into the palm of one's hand," said Lt. Cmdr. Theron Hamilton, one of the NMRC researchers involved in the development of EDGE.

"This makes it a very useful tool for clinical and force health protection applications," said Hamilton. "One of the main goals behind developing EDGE was to find a way to enable the analysis of sequence data closer to where the samples are collected, so faster collection of actionable information could be used to support the warfighter."

Laboratories across the world, including clinical and university laboratories, have started to adopt high-throughput sequencing with this advanced technology, but there is a caveat. Hamilton

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explained, “Many laboratories new to high-throughput sequencing are ill-equipped to analyze the enormous amounts of data the instrument is capable of producing, both from the standpoint of computational hardware and bioinformatics expertise.”

To combat this problem, EDGE is designed to run on small, portable and relatively inexpensive hardware that makes bioinformatic analyses user friendly by providing an intuitive web-based interface for scientists to analyst high-throughput sequence data.

According to Hamilton, EDGE is the only freely available, open-source bioinformatic software platform that can be run locally without internet, and enables the user to perform quality control of sequence data, host removal, genome assembly and annotation, comparisons to reference genomes, taxonomic profiling, phylogenetic analyses, as well as primer design.

A poster on EDGE will be presented at the American Society for Microbiology (ASM) Microbe, June 1-5, 2017, in New Orleans, Louisiana. The software and associated databases is public, see: <https://github.com/LANL-Bioinformatics/EDGE>, and a demonstration web server, <https://bioedge.lanl.gov>, is available for use with publicly available data.

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